

Sbjct: 898 ctggtactgccagatccagtaccggcccttctttccctgaccgccactctgggctggc 957

Query: 758 cggcttcaccctgctcctcagtcctcctggcctttgccatgtaccgcccglagtgcctccg 817
 |||

Sbjct: 958 cggcttcaccctgctcctcagtcctcctggcctttgccatgtaccgcccglagtgcctccg 1017

Query: 818 cgggcgcttggcagcgctcgccggccctcctcgacattgctccccgcgcgcggcgaggc 877
 |||

Sbjct: 1018 cgggcgcttggcagcgctcgccggccctcctcgacattgctccccgcgcgcggcgaggc 1077

Query: 878 tgetgcctgcccaggcccgccctctccggcctgcctcttcccgctgcctggagcccagcc 937
 |||

Sbjct: 1078 tgetgcctgcccaggcccgccctctccggcctgcctcttcccgctgcctggagcccagcc 1137

Query: 938 ctgcgcgcagaggactcccgaggactggcggaggccccgcctgacacgcgcggggctcg 997
 |||

Sbjct: 1138 ctgcgcgcagaggactcccgaggactggcggaggccccgcctgacacgcgcggggctcg 1197

Query: 998 gggccacctcccggggctgctgmcc-tcagcccgcaactgggagtgggctcctcggggtcg 1056
 |||

Sbjct: 1198 gggccacctcccggggctgctgacctcagcccgcaactgggagtgggctcctcggggtcg 1257

Query: 1057 ggcattctgtgctgctgcctcgcccccgggcagagccggggcccccgggggcccgtctt 1116
 |||

Sbjct: 1258 ggcattctgtgctgctgcctcgcccccgggcagagccggggcccccgggggcccgtctt 1317

Query: 1117 agtgttctgcccaggagaccagccgcctccm-tccclgacagctccttgggctgagttgg 1175
 |||

Sbjct: 1318 agtgttctgcccaggagaccagccgcctccaatccctgacagctccttgggctgagttgg 1377

Query: 1176 ggacgccaggctcggctgggaggctggtgm-ggggagcggggaggggagaggagttccccg 1234
 |||

Sbjct: 1378 ggacgccaggctcggctgggaggctggtgaaggggagcggggaggggagaggagttccccg 1437

Query: 1235 gm-cccgtgcagattw--gtm-ctgtgm-glitttaaaaaaaaaaaaaaaaaaaaa 1281
 | |||

Sbjct: 1438 gaaccctgagattaaagtaactgtgaagttttcaaaaaaaaaaaaaaaaaaaaa 1489

Score = 36.6 bits (18), Expect = 125
 Identities = 18/18 (100%)
 Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281
 |||


Sbjct: 1477 aaaaaaaaaaaaaaaaaaaaaa 1494

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281
|||||||
Sbjct: 1476 aaaaaaaaaaaaaaaaaaaaaa 1493

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281
|||||||
Sbjct: 1475 aaaaaaaaaaaaaaaaaaaaaa 1492

>gi|31543199|ref|NM_031434.2|  Homo sapiens chromosome 7 open reading frame 2
Length = 1494

Score = 2042 bits (1019), Expect = 0.0
Identities = 1203/1252 (96%), Gaps = 28/1252 (2%)
Strand = Plus / Plus

Query: 58 gctcggtagcgcggcggggcm-ggcaggcgccatgaccctgattgm-ggggtgggtgatga 115
|||||||
Sbjct: 238 gctcggtagcgcggcgggcaaggcaggcgccatgaccctgattgaaggggtggglgatga 297

Query: 116 ggtgaccgtccttttctcggtgcttgccctgccttctggtgctggcccttgccctgggtctc 175
|||||||
Sbjct: 298 ggtgaccgtccttttctcggtgcttgccctgccttctggtgctggcccttgccctgggtctc 357

Query: 176 m-cgcacaccgctgagggcggggacccactgccccagccgtcagggaccccm-cgccatc 233
|||||||
Sbjct: 358 aacgcacaccgctgagggcggggacccactgccccagccgtcagggaccccaacgccatc 417

Query: 234 ccagcccagcgcagccatggcagctaccgacagcatgagaggggaggccccaggggcaga 293
|||||||
Sbjct: 418 ccagcccagcgcagccatggcagctaccgacagcatgagaggggaggccccaggggcaga 477

Query: 294 gacccccagcctgagacacagaggtcm-gctgcacagccagagcccagcacggggttcac 352
|||||||
Sbjct: 478 gacccccagcctgagacacagaggtcaagctgcacagccagagcccagcacggggttcac 537

Query: 353 agcm-caccgccagccccggactccccgcaggagccccctcgtgctacggctgw--ttcct 409
||| |||||
Sbjct: 538 agcaacaccgccagccccggactccccgcaggagccccctcgtgctacggctgaaattcct 597

Query: 1117 agtgttctgcccggaggaccagccgcctccm-tccctgacagctccttgggctgagttgg 1175
 |||
 Sbjct: 1318 agtgttctgcccggaggaccagccgcctccaatccctgacagctccttgggctgagttgg 1377

Query: 1176 ggacgccaggtcgggtgggaggctggtgm-ggggagcggggaggggcagaggagttccccg 1234
 |||
 Sbjct: 1378 ggacgccaggtcgggtgggaggctggtgaaggggagcggggaggggcagaggagttccccg 1437

Query: 1235 gm-cccgtgcagattw---gtm-ctgtgm-gttttaaaaaaaaaaaaaaaaaaaaa 1281
 | |||
 Sbjct: 1438 gaaccctgagattaaagtaactgtgaagttttcaaaaaaaaaaaaaaaaaaaaaa 1489

Score = 36.6 bits (18), Expect = 125
 Identities = 18/18 (100%)
 Strand = Plus / Plus


Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281
 |||
 Sbjct: 1477 aaaaaaaaaaaaaaaaaaaaaa 1494

Score = 36.6 bits (18), Expect = 125
 Identities = 18/18 (100%)
 Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281
 |||
 Sbjct: 1476 aaaaaaaaaaaaaaaaaaaaaa 1493

Score = 36.6 bits (18), Expect = 125
 Identities = 18/18 (100%)
 Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281
 |||
 Sbjct: 1475 aaaaaaaaaaaaaaaaaaaaaa 1492

>gi|16756334|gb|AC010973.6|  Homo sapiens BAC clone RP11-148K1 from 7, complete s
 Length = 222605

Score = 1395 bits (696), Expect = 0.0
 Identities = 775/796 (97%), Gaps = 11/796 (1%)
 Strand = Plus / Plus

Query: 464 ggacccagtttcccgccggg-mcagcaggtgcgactcatctacc-mgggcagctgctag 521
 |||
 Sbjct: 123794 ggacccagtttcccgccgggaacagcaggtgcgactcatclaccaagggcagctgctag 123853

Query: 522 ggcagacacccagaccctgggcagccttcacctccctccc-mctgcgttctccactgcc 580
|||||
Sbjct: 123854 ggcagacacccagaccctgggcagccttcacctccctcccaactgcgttctccactgcc 123913

Query: 581 acgtgtccacgagagtcgggtccccc--wtccccctgcccgcgggggtccgagcccggcc 638
|||||
Sbjct: 123914 acgtgtccacgagagtcgggtccccc aaatccccctgcccgcgggggtccgagcccggcc 123973

Query: 639 cctccgggctgg--wtccggcagcctgctgctgcccctgctgctcctgctgttgctgctgc 696
|||||
Sbjct: 123974 cctccgggctggaaatccggcagcctgctgctgcccctgctgctcctgctgttgctgctgc 124033

Query: 697 tctgggtactgccagatccagtagccgccccttctttcccctgaccgccactctgggcctgg 756
|||||
Sbjct: 124034 tctgggtactgccagatccagtagccgccccttctttcccctgaccgccactctgggcctgg 124093

Query: 757 ccggcttcaccctgctcctcagtcctcctggcctttgccatgtaccgcccgtagtgccctcc 816
|||||
Sbjct: 124094 ccggcttcaccctgctcctcagtcctcctggcctttgccatgtaccgcccgtagtgccctcc 124153

Query: 817 gcgggcgcttggcagcgtcgcggccctccggaccttgctccccgcgcgcggcgaggag 876
|||||
Sbjct: 124154 gcgggcgcttggcagcgtcgcggccctccggaccttgctccccgcgcgcggcgaggag 124213

Query: 877 ctgctgcctgccagggccgcctctccggcctgcctcttcccgcctggagcccagc 936
|||||
Sbjct: 124214 ctgctgcctgccagggccgcctctccggcctgcctcttcccgcctggagcccagc 124273

Query: 937 cctgcgcgcagaggactcccgggactggcgaggccccgcctgcgaccgcgggggctc 996
|||||
Sbjct: 124274 cctgcgcgcagaggactcccgggactggcgaggccccgcctgcgaccgcgggggctc 124333

Query: 997 ggggccacctccgggggtgctg-mcctcagcccgcaactgggagtgggctcctcgggggtc 1055
|||||
Sbjct: 124334 ggggccacctccgggggtgctgacctcagcccgcaactgggagtgggctcctcgggggtc 124393

Query: 1056 gggcatctgctgtcgtgcctcgccccgggcagagccggggccgccccggggggccgtct 1115
|||||
Sbjct: 124394 gggcatctgctgtcgtgcctcgccccgggcagagccggggccgccccggggggccgtct 124453

Query: 1116 tagtggtctgcccggaggaccagccgcctcc-mtccctgacagctccttgggctgagttg 1174
|||||
Sbjct: 124454 tagtggtctgcccggaggaccagccgcctccaatccctgacagctccttgggctgagttg 124513

Query: 1175 gggacgccaggtcgggtgggaggctggtg-mggggagcggggaggggcagaggagttcccc 1233
|||||
Sbjct: 124514 gggacgccaggtcgggtgggaggctggtgaaggggagcggggaggggcagaggagttcccc 124573

Query: 1234 gg-mcccgtgcagatt 1248
|| |||||
Sbjct: 124574 ggaacccgtgcagatt 124589

Score = 665 bits (332), Expect = 0.0
Identities = 398/415 (95%), Gaps = 9/415 (2%)
Strand = Plus / Plus

Query: 58 gctcggtagcgcggcgggcm-ggcaggcgccatgaccctgattgm-ggggtgggtgatga 115
|||||
Sbjct: 123101 gctcggtagcgcggcgggcaaggcaggcgccatgaccctgattgaaggggtgggtgatga 123160

Query: 116 ggtgaccgtcctttttctcgggtgcttgccctgccttctggtgctggcccttgccctgggtctc 175
|||||
Sbjct: 123161 ggtgaccgtcctttttctcgggtgcttgccctgccttctggtgctggcccttgccctgggtctc 123220

Query: 176 m-cgcacaccgctgagggcggggacccactgccccagccgtcagggaccccm-cgccatc 233
|||||
Sbjct: 123221 aacgcacaccgctgagggcggggacccactgccccagccgtcagggaccccaacgccatc 123280

Query: 234 ccagcccagcgcagccatggcagctaccgacagcatgagaggggaggccccaggggcaga 293
|||||
Sbjct: 123281 ccagcccagcgcagccatggcagctaccgacagcatgagaggggaggccccaggggcaga 123340

Query: 294 gacccccagcctgagacacagaggtc-mgctgcacagccagagccagcacgggggttcac 352
|||||
Sbjct: 123341 gacccccagcctgagacacagaggtaagctgcacagccagagccagcacgggggttcac 123400

Query: 353 agc-mcaccgccagccccggactccccgcaggagccccctcgtgctacggctg--wtccct 409
||| |||||
Sbjct: 123401 agcaacacccgccagccccggactccccgcaggagccccctcgtgctacggctgaaattcct 123460

Query: 410 c-mtgattcagagcaggtggccagggcctggccccacgacaccattggctccttg 463
| |||||
Sbjct: 123461 caatgattcagagcaggtggccagggcctggccccacgacaccattggctccttg 123515

Score = 80.7 bits (40), Expect = 7e-12
Identities = 48/50 (96%), Gaps = 1/50 (2%)
Strand = Plus / Plus

Query: 10 cccgcccggm-gtgcccagaggggcccgcgatggagctgggggagccgggcg 58
|||||
Sbjct: 122212 cccgcccgaagtgcggcagaggggcccgcgatggagctgggggagccgggcg 122261

Score = 42.6 bits (21), Expect = 1.9
Identities = 21/21 (100%)
Strand = Plus / Plus

Query: 1261 ttttaaaaaaaaaaaaaaaaaaaaa 1281
|||||
Sbjct: 115287 ttttaaaaaaaaaaaaaaaaaaaaa 115307

Score = 38.6 bits (19), Expect = 31
Identities = 22/23 (95%)
Strand = Plus / Plus

Query: 1259 gtttttaaaaaaaaaaaaaaaaaaaaa 1281
|||||
Sbjct: 115286 gtttttaaaaaaaaaaaaaaaaaaaaa 115308

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281
|||||
Sbjct: 218391 aaaaaaaaaaaaaaaaaaaaaa 218374

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281
|||||
Sbjct: 218390 aaaaaaaaaaaaaaaaaaaaaa 218373

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaaaaaa 1281
|||||
Sbjct: 218389 aaaaaaaaaaaaaaaaaaaaaa 218372

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281
 |||||
 Sbjct: 136554 aaaaaaaaaaaaaaaaaa 136537

Score = 36.6 bits (18), Expect = 125
 Identities = 18/18 (100%)
 Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281
 |||||
 Sbjct: 136553 aaaaaaaaaaaaaaaaaa 136536

Score = 36.6 bits (18), Expect = 125
 Identities = 18/18 (100%)
 Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281
 |||||
 Sbjct: 115297 aaaaaaaaaaaaaaaaaa 115314

Score = 36.6 bits (18), Expect = 125
 Identities = 18/18 (100%)
 Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281
 |||||
 Sbjct: 115296 aaaaaaaaaaaaaaaaaa 115313

Score = 36.6 bits (18), Expect = 125
 Identities = 18/18 (100%)
 Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281
 |||||
 Sbjct: 115295 aaaaaaaaaaaaaaaaaa 115312

Score = 36.6 bits (18), Expect = 125
 Identities = 18/18 (100%)
 Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281
 |||||
 Sbjct: 115294 aaaaaaaaaaaaaaaaaa 115311

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaaaa 1281
|||||||
Sbjct: 115293 aaaaaaaaaaaaaaaaaaaa 115310

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Plus

Query: 1264 aaaaaaaaaaaaaaaaaaaa 1281
|||||||
Sbjct: 115292 aaaaaaaaaaaaaaaaaaaa 115309

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaaaa 1281
|||||||
Sbjct: 109993 aaaaaaaaaaaaaaaaaaaa 109976

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaaaa 1281
|||||||
Sbjct: 109992 aaaaaaaaaaaaaaaaaaaa 109975

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaaaa 1281
|||||||
Sbjct: 109991 aaaaaaaaaaaaaaaaaaaa 109974

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281
|||||||
Sbjct: 109990 aaaaaaaaaaaaaaaaaa 109973

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281
|||||||
Sbjct: 109989 aaaaaaaaaaaaaaaaaa 109972

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281
|||||||
Sbjct: 109988 aaaaaaaaaaaaaaaaaa 109971

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281
|||||||
Sbjct: 109987 aaaaaaaaaaaaaaaaaa 109970

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281
|||||||
Sbjct: 109986 aaaaaaaaaaaaaaaaaa 109969

Score = 36.6 bits (18), Expect = 125
Identities = 18/18 (100%)
Strand = Plus / Minus

Query: 1264 aaaaaaaaaaaaaaaaaa 1281
|||||||
Sbjct: 109985 aaaaaaaaaaaaaaaaaa 109968

**BLASTN 2.2.8 [Jan-05-2004]**Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1079554228-18277-13018448633.BLASTQ3

Query=

(1281 letters)

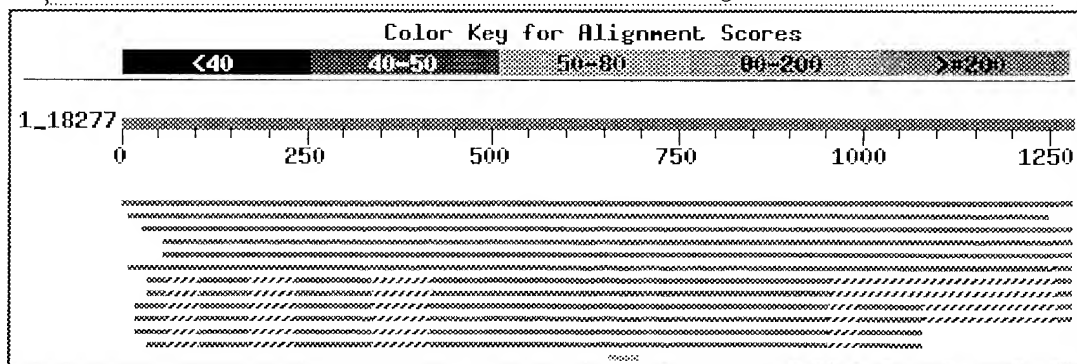
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)

2,102,977 sequences; 10,130,642,339 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

Taxonomy reports**Distribution of 3783 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gi 37182084 gb AY358481.1 	Homo sapiens clone DNA73744 TLIE...	2146	0.0	
gi 12654232 gb BC000936.1 	Homo sapiens chromosome 7 open r...	2112	0.0	
gi 21303410 gb AY037155.1 	Homo sapiens hypothetical membra...	2102	0.0	
gi 21620057 gb BC033182.1 	Homo sapiens chromosome 7 open r...	2042	0.0	
gi 31543199 ref NM_031434.2 	Homo sapiens chromosome 7 open...	2042	0.0	

gi 16756334 gb AC010973.6 	Homo sapiens BAC clone RP11-148K...	1395	0.0	
gi 37589845 gb BC059162.1 	Rattus norvegicus Unknown (prote...	509	e-141	
gi 38454297 ref NM_198781.1 	Rattus norvegicus Unknown (pro...	509	e-141	
gi 18043423 gb BC019547.1 	Mus musculus RIKEN cDNA 20100040...	463	e-127	
gi 12842087 dbj AK008109.1 	Mus musculus adult male small i...	463	e-127	
gi 7259235 dbj AB030183.1 	Mus musculus mRNA, complete cds,...	463	e-127	
gi 11967944 ref NM_022418.1 	Mus musculus RIKEN cDNA 201000...	463	e-127	
gi 2961613 gb AF051726.1 MMCATS1	Mus musculus cathepsin S (...)	63	2e-06	
gi 18873502 emb AL603702.14 	Mouse DNA sequence from clone ...	63	2e-06	
gi 21953265 emb AL591913.14 	Mouse DNA sequence from clone ...	63	2e-06	
gi 25013379 gb AC092203.16 	Mus musculus chromosome 3 clone...	61	7e-06	
gi 20068539 emb AL606742.11 	Mouse DNA sequence from clone ...	61	7e-06	
gi 22832231 gb AE003496.3 	Drosophila melanogaster chromoso...	59	3e-05	
gi 23172508 gb AE003766.2 	Drosophila melanogaster chromoso...	59	3e-05	
gi 15451484 gb AC022346.3 	Drosophila melanogaster, chromos...	59	3e-05	
gi 14028963 gb AC022343.2 AC022343	Drosophila melanogaster,...	59	3e-05	
gi 13676919 gb AC007827.5 AC007827	Drosophila melanogaster,...	59	3e-05	
gi 25455625 gb BC040122.1 	Homo sapiens paired immunogloblin...	57	1e-04	
gi 29791641 gb BC050547.1 	Homo sapiens paired immunogloblin...	57	1e-04	
gi 37361058 gb AC107662.9 	Mus musculus chromosome 9, clone...	57	1e-04	
gi 16551810 dbj AK056412.1 	Homo sapiens cDNA FLJ31850 fis,...	57	1e-04	
gi 20800363 gb AC025627.13 	Homo sapiens chromosome 17, clo...	57	1e-04	
gi 28201706 gb AC004448.3 	Homo sapiens chromosome 17, clon...	57	1e-04	
gi 5817856 gb AF161081.1 AF161081	Homo sapiens activating r...	57	1e-04	
gi 4508112 gb AC005071.2 AC005071	Homo sapiens clone RG161A...	57	1e-04	
gi 10441892 gb AF217981.1 AF217981	Homo sapiens clone PP155...	57	1e-04	
gi 6706622 emb AJ279565.1 HSA279565	Homo sapiens genomic DN...	57	1e-04	
gi 21739966 emb AL834336.1 HSM805391	Homo sapiens mRNA; cDN...	57	1e-04	
gi 21739928 emb AL834317.1 HSM805361	Homo sapiens mRNA; cDN...	57	1e-04	
gi 11932154 emb AJ400846.1 HSA400846	Homo sapiens mRNA for ...	57	1e-04	
gi 11932151 emb AJ400845.1 HSA400845	Homo sapiens mRNA for ...	57	1e-04	
gi 206982 gb M32515.1 RATSIMPB	Rat simple sequence DNA, clo...	57	1e-04	
gi 206979 gb M36626.1 RATSIMPA1	Rat simple sequence DNA, cl...	57	1e-04	
gi 30179910 ref NM_178238.1 	Homo sapiens paired immunoglob...	57	1e-04	
gi 30179914 ref NM_013440.3 	Homo sapiens paired immunoglob...	57	1e-04	
gi 30179912 ref NM_175047.2 	Homo sapiens paired immunoglob...	57	1e-04	
gi 38564373 gb AC113203.10 	Mus musculus chromosome 5, clon...	55	5e-04	
gi 33147431 gb AC127256.4 	Mus musculus BAC clone RP24-296G...	55	5e-04	
gi 18043222 gb BC020026.1 	Mus musculus cell division cycle...	55	5e-04	
gi 22213506 gb AC122857.2 	Mus musculus BAC clone RP23-125A...	55	5e-04	
gi 22138609 gb AC121903.2 	Mus musculus BAC clone RP24-174G...	55	5e-04	
gi 37951419 gb AC110240.8 	Mus musculus chromosome 3, clone...	55	5e-04	
gi 32421368 ref XM_331127.1 	Neurospora crassa strain OR74A	55	5e-04	
gi 7656273 gb AC067939.1 AC067939	Neurospora crassa chromos...	55	5e-04	
gi 20068407 emb AL358472.54 	Human DNA sequence from clone ...	55	5e-04	
gi 6715147 gb AF188622.1 AF188622	Mus musculus selectively ...	55	5e-04	
gi 42656116 ref XM_375806.1 	Homo sapiens KIAA0476 gene pro...	55	5e-04	
gi 32436422 emb AL935159.11 	Mouse DNA sequence from clone ...	55	5e-04	
gi 10946743 ref NM_021398.1 	Mus musculus solute carrier fa...	55	5e-04	
gi 41351569 gb AC110219.11 	Mus musculus chromosome 1, clon...	55	5e-04	
gi 40557568 gb AY489267.1 	Pinus sylvestris microsatellite ...	55	5e-04	

gi 21614629 emb AL672218.9 	Mouse DNA sequence from clone R...	55	5e-04	
gi 38050 emb X68361.1 MFAP0A4A	M.fascicularis gene for apol...	55	5e-04	
gi 307289 gb L10375.1 HUMMRNAD	Human (clone CTG-B10) mRNA s...	55	5e-04	
gi 34576915 gb AY368204.1 	Homo sapiens TATA box binding pr...	53	0.002	
gi 33439371 gb AY333202.1 	Anopheles merus clone r2a micros...	53	0.002	
gi 33439365 gb AY333196.1 	Anopheles gambiae clone b2bc mic...	53	0.002	
gi 33439364 gb AY333195.1 	Anopheles gambiae clone b2a micr...	53	0.002	
gi 33439363 gb AY333194.1 	Anopheles gambiae clone b1bc mic...	52	0.002	
gi 33439362 gb AY333193.1 	Anopheles gambiae clone b1a micr...	53	0.002	
gi 33439361 gb AY333192.1 	Anopheles gambiae clone s2ab mic...	53	0.002	
gi 33439360 gb AY333191.1 	Anopheles gambiae clone s1ab mic...	53	0.002	
gi 14318643 gb BC009120.1 	Mus musculus hypothetical protei...	53	0.002	
gi 23124364 gb AC093043.6 	Mus Musculus Strain C57BL6/J Chr...	53	0.002	
gi 29423846 gb AC137055.12 	Homo sapiens 12 BAC RP11-686G8 ...	53	0.002	
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gi 40354196 ref NM_020457.2 	Homo sapiens THAP domain conta...	53	0.002	

Alignments

Get selected sequences

Select all

Deselect all

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Score = 2146 bits (1071), Expect = 0.0
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

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

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Strand = Plus / Plus

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